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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 19, 2002, 19:19:31 ; Search time 344.5 Seconds
(without alignments)
10434.731 Million cell updates/sec

Title: US-09-731-457B-3
Perfect score: 4193
Sequence: 1 gtggagttcgctgcggctgt.....agttttaccaaataaagtag 4193

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 0

Total number of hits satisfying chosen parameters: 989696

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	28	0.7	39	18	AAT65714	Repeat sequence fr
	2	28	0.7	48	21	AAA77335	Human clone cg4402
	3	28	0.7	50	13	AAQ34003	Microsatellite seq
c	4	27	0.6	45	18	AAT65737	Repeat sequence fr
	5	26	0.6	29	13	AAQ33630	Microsatellite seq
	6	25	0.6	35	13	AAQ33713	Microsatellite seq
	7	25	0.6	44	21	AAA77337	Human clone cg4402
c	8	24	0.6	40	18	AAT65736	Repeat sequence fr
c	9	23	0.5	50	18	AAT65741	Repeat sequence fr
	10	22	0.5	27	13	AAQ34077	Microsatellite seq
	11	21	0.5	24	22	AAH39357	SNP specific upper
c	12	21	0.5	40	18	AAT65743	Repeat sequence fr
c	13	20	0.5	20	16	AAQ82617	Chromosome 11 (loc
	14	20	0.5	20	16	AAQ82618	Chromosome 11 (loc
c	15	20	0.5	21	18	AAT58080	ICAM-1 antisense o
c	16	20	0.5	21	19	AAV38616	Human ICAM-1, E-se
	17	19	0.5	27	21	AAA80358	Human ASTH1I 5' re
	18	19	0.5	35	13	AAQ33695	Microsatellite seq
	19	19	0.5	37	13	AAQ33669	Microsatellite seq
c	20	19	0.5	46	18	AAT65709	Repeat sequence fr
	21	19	0.5	50	13	AAQ34167	Sequence of a micr
c	22	18	0.4	24	14	AAQ40668	tPA-12 in vitro mu
c	23	18	0.4	30	21	AAZ98502	H. discus derived
	24	18	0.4	32	13	AAQ34119	Sequence of a micr
	25	18	0.4	37	13	AAQ33698	Microsatellite seq
c	26	18	0.4	43	18	AAT65788	Repeat sequence fr
c	27	18	0.4	44	21	AAZ98507	H. discus derived
	28	17	0.4	23	21	AAA80357	Human ASTH1I 5' re
c	29	17	0.4	25	21	AAZ92012	Mahogany protein g
	30	17	0.4	40	13	AAQ34094	Sequence of a micr
c	31	17	0.4	40	21	AAZ98493	H. discus derived
c	32	17	0.4	42	18	AAT65797	Repeat sequence fr
c	33	17	0.4	47	21	AAZ68141	Human map-related
	34	17	0.4	49	13	AAQ34122	Sequence of a micr
	35	16	0.4	19	17	AAT30412	Compound simple se
c	36	16	0.4	19	19	AAV41067	Primer TEL:114U19
c	37	16	0.4	20	14	AAQ48546	HPV E6/7 region pr
c	38	16	0.4	20	17	AAT30427	Compound simple se
	39	16	0.4	20	22	AAS09069	Human MEKK2 antise
c	40	16	0.4	23	22	AAC83579	Human FMR1 gene tr
c	41	16	0.4	24	21	AAZ98498	H. discus derived
	42	16	0.4	26	13	AAQ34131	Sequence of a micr
	43	16	0.4	27	13	AAQ33740	Microsatellite seq
c	44	16	0.4	27	22	AAI61970	Soybean 240017 reg
	45	16	0.4	34	13	AAQ33761	Microsatellite seq

ALIGNMENTS

RESULT 1
AAT65714/c
ID AAT65714 standard; DNA; 39 BP.
XX
AC AAT65714;
XX
DT 17-JUN-1997 (first entry)
XX
DE Repeat sequence from polymorphic marker clone Mfd12.
XX
KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW linkage analysis; genetic disease; animal; plant; breeding; locus;
KW hybridisation; chromosome; ds.
XX
OS Homo sapiens.
XX
PN US5582979-A.
XX
PD 10-DEC-1996.
XX
PF 21-APR-1989; 89US-0341562.
XX
PR 05-SEP-1991; 91US-0754351.
PR 21-APR-1989; 89US-0341562.
PR 04-APR-1994; 94US-0222177.
XX
PA (MARS-) MARSHFIELD CLINIC.
XX
PI Weber JL;
XX
DR WPI; 1997-042299/04.
XX
PT Detection of polymorphic genetic markers of the form

```
PT   (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
XX
PS   Disclosure; Column 9-10; 186pp; English.
XX
CC   The invention relates to the isolation of polymorphic repeat sequences
CC   having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC   markers.  Primers based on these sequences can be used to detect these
CC   repeats, especially for use in e.g paternity or maternity testing,
CC   human genetic analysis such as linkage analysis of genetic disease,
CC   commercial animal or plant breeding or pedigree analysis.  Clones
CC   containing the repeat sequences were isolated by hybridisation of
CC   chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC   probe.  Over 100 repeat blocks were isolated. The inserts from the
CC   clones were amplified by primers AAT65798-T66047.  Those clones where the
CC   repeat sequence has been determined are shown in AAT65704-797.  This
CC   repeat sequence is from the marker clone Mdf12 which contains the repeat
CC   sequence having the formula: (AC)11AT(AC)8A.
XX
SQ   Sequence 39 BP; 20 A; 18 C; 0 G; 1 T; 0 other;


  Query Match             0.7%;  Score 28;  DB 18;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgtgtgtgtgtgt 3876
           ||||||||||||||||||||||||||||
Db     36 GTGTGTGTGTGTGTATGTGTGTGTGTGT 9


RESULT   2
AAA77335
ID   AAA77335 standard; cDNA; 48 BP.
XX
AC   AAA77335;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Human clone cg44024536 polymorphic site, SEQ ID NO:1018.
XX
KW   Human; single nucleotide polymorphism; SNP; chromosome 9;
KW   detection; identification; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace (26,G)
FT                   /*tag= a
XX
PN   WO200029623-A2.
XX
PD   25-MAY-2000.
XX
PF   17-NOV-1999;   99WO-US27293.
XX
PR   17-NOV-1998;   98US-0109024.
PR   16-NOV-1999;   99US-0109024.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach MD;
XX
DR   WPI; 2000-387826/33.
XX
PT   Human nucleic acids containing single nucleotide polymorphisms, useful
PT   for treating a subject suffering, or at risk from a pathology due to
PT   the presence of a sequence polymorphism -
XX
PS   Claim 1; Page 466; 543pp; English.
XX
CC   Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC   which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC   1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
CC   contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
CC   consecutive pairs of nucleotides containing SNPs which result in changes
CC   in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC   sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC   changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC   in non- conservative changes. The SNPs in sequences 1187 to 1192
CC   (AAA77504-A77509) generate frameshift mutations. The invention also
CC   relates to a method of detecting a polymorphic site in a nucleic acid and
CC   a method of determining the relatedness of two nucleic acids. It also
CC   encompasses peptides containing polymorphic sites, antibodies raised
CC   against such peptides, and a method of detecting polymorphic
CC   proteins/peptides using the antibodies. The nucleic acids are useful for
CC   gene therapy of an individual having, suspected of having, or at risk of
CC   developing a pathological condition due to the presence of a sequence
CC   polymorphism. Such treatment would comprise administration of the
CC   wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC   peptides can also be used in the treatment of such individuals.
XX
SQ   Sequence 48 BP; 2 A; 2 C; 24 G; 20 T; 0 other;


  Query Match             0.7%;  Score 28;  DB 21;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgtgtgtgtgtgt 3876
           ||||||||||||||||||||||||||||
Db     12 gtgtgtgtgtgtgtatgtgtgtgtgtgt 39


RESULT   3
AAQ34003
ID   AAQ34003 standard; DNA; 50 BP.
XX
AC   AAQ34003;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone TGLA400.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 331; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised.  Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000.  The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
```

```
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM).  The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 50 BP; 1 A; 2 C; 22 G; 25 T; 0 other;


  Query Match             0.7%;  Score 28;  DB 13;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgtgtgtgtgtgt 3876
            ||||||||||||||||||||||||||||
Db     11 gtgtgtgtgtgtgtatgtgtgtgtgtgt 38


RESULT   4
AAT65737/c
ID   AAT65737 standard; DNA; 45 BP.
XX
AC   AAT65737;
XX
DT   17-JUN-1997  (first entry)
XX
DE   Repeat sequence from polymorphic marker clone Mfd36.
XX
KW   Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW   PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW   linkage analysis; genetic disease; animal; plant; breeding; locus;
KW   hybridisation; chromosome; ds.
XX
OS   Homo sapiens.
XX
PN   US5582979-A.
XX
PD   10-DEC-1996.
XX
PF   21-APR-1989;   89US-0341562.
XX
PR   05-SEP-1991;   91US-0754351.
PR   21-APR-1989;   89US-0341562.
PR   04-APR-1994;   94US-0222177.
XX
PA   (MARS-) MARSHFIELD CLINIC.
XX
PI   Weber JL;
XX
DR   WPI; 1997-042299/04.
XX
PT   Detection of polymorphic genetic markers of the form
PT   (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
XX
PS   Disclosure; Column 9-10; 186pp; English.
XX
CC   The invention relates to the isolation of polymorphic repeat sequences
CC   having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC   markers.  Primers based on these sequences can be used to detect these
CC   repeats, especially for use in e.g paternity or maternity testing,
CC   human genetic analysis such as linkage analysis of genetic disease,
CC   commercial animal or plant breeding or pedigree analysis.  Clones
CC   containing the repeat sequences were isolated by hybridisation of
CC   chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC   probe.  Over 100 repeat blocks were isolated. The inserts from the
CC   clones were amplified by primers AAT65798-T66047.  Those clones where the
CC   repeat sequence has been determined are shown in AAT65704-797.  This
CC   repeat sequence is from the marker clone Mdf36 which contains the repeat
CC   sequence having the formula: (AC)15AT(AC)6A.
XX
SQ   Sequence 45 BP; 23 A; 21 C; 0 G; 1 T; 0 other;


  Query Match             0.6%;  Score 27;  DB 18;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3850 tgtgtgtgtgtgtatgtgtgtgtgtgt 3876
            |||||||||||||||||||||||||||
Db     45 TGTGTGTGTGTGTATGTGTGTGTGTGT 19


RESULT   5
AAQ33630
ID   AAQ33630 standard; DNA; 29 BP.
XX
AC   AAQ33630;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone GBPRLGR.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 181; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised.  Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000.  The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM).  The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 29 BP; 1 A; 0 C; 13 G; 15 T; 0 other;


  Query Match             0.6%;  Score 26;  DB 13;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3850 tgtgtgtgtgtgtatgtgtgtgtgtg 3875
            ||||||||||||||||||||||||||
Db      4 tgtgtgtgtgtgtatgtgtgtgtgtg 29
```

```
RESULT   6
AAQ33713
ID   AAQ33713 standard; DNA; 35 BP.
XX
AC   AAQ33713;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone TGLA134.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 215; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised.  Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000.  The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM).  The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 35 BP; 1 A; 0 C; 17 G; 17 T; 0 other;

  Query Match             0.6%;  Score 25;  DB 13;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgtgtgtgtg 3873
         |||||||||||||||||||||||||
Db     11 gtgtgtgtgtgtgtatgtgtgtgtg 35


RESULT   7
AAA77337
ID   AAA77337 standard; cDNA; 44 BP.
XX
AC   AAA77337;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Human clone cg44024536 polymorphic site, SEQ ID NO:1020.
XX
KW   Human; single nucleotide polymorphism; SNP; chromosome 9;
KW   detection; identification; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace (26,G)
FT                   /*tag= a
XX
PN   WO200029623-A2.
XX
PD   25-MAY-2000.
XX
PF   17-NOV-1999;   99WO-US27293.
XX
PR   17-NOV-1998;   98US-0109024.
PR   16-NOV-1999;   99US-0109024.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach MD;
XX
DR   WPI; 2000-387826/33.
XX
PT   Human nucleic acids containing single nucleotide polymorphisms, useful
PT   for treating a subject suffering, or at risk from a pathology due to
PT   the presence of a sequence polymorphism -
XX
PS   Claim 1; Page 466; 543pp; English.
XX
CC   Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC   which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC   1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
CC   contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
CC   consecutive pairs of nucleotides containing SNPs which result in changes
CC   in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC   sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC   changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC   in non- conservative changes. The SNPs in sequences 1187 to 1192
CC   (AAA77504-A77509) generate frameshift mutations. The invention also
CC   relates to a method of detecting a polymorphic site in a nucleic acid and
CC   a method of determining the relatedness of two nucleic acids. It also
CC   encompasses peptides containing polymorphic sites, antibodies raised
CC   against such peptides, and a method of detecting polymorphic
CC   proteins/peptides using the antibodies. The nucleic acids are useful for
CC   gene therapy of an individual having, suspected of having, or at risk of
CC   developing a pathological condition due to the presence of a sequence
CC   polymorphism. Such treatment would comprise administration of the
CC   wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC   peptides can also be used in the treatment of such individuals.
XX
SQ   Sequence 44 BP; 1 A; 2 C; 21 G; 20 T; 0 other;

  Query Match             0.6%;  Score 25;  DB 21;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgtgtgtgtg 3873
         |||||||||||||||||||||||||
Db     12 gtgtgtgtgtgtgtatgtgtgtgtg 36


RESULT   8
AAT65736/c
ID   AAT65736 standard; DNA; 40 BP.
XX
AC   AAT65736;
XX
DT   17-JUN-1997  (first entry)
XX
DE   Repeat sequence from polymorphic marker clone Mfd34.
```

```
XX
KW   Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW   PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW   linkage analysis; genetic disease; animal; plant; breeding; locus;
KW   hybridisation; chromosome; ds.
XX
OS   Homo sapiens.
XX
PN   US5582979-A.
XX
PD   10-DEC-1996.
XX
PF   21-APR-1989;   89US-0341562.
XX
PR   05-SEP-1991;   91US-0754351.
PR   21-APR-1989;   89US-0341562.
PR   04-APR-1994;   94US-0222177.
XX
PA   (MARS-) MARSHFIELD CLINIC.
XX
PI   Weber JL;
XX
DR   WPI; 1997-042299/04.
XX
PT   Detection of polymorphic genetic markers of the form
PT   (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
XX
PS   Disclosure; Column 9-10; 186pp; English.
XX
CC   The invention relates to the isolation of polymorphic repeat sequences
CC   having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC   markers.  Primers based on these sequences can be used to detect these
CC   repeats, especially for use in e.g paternity or maternity testing,
CC   human genetic analysis such as linkage analysis of genetic disease,
CC   commercial animal or plant breeding or pedigree analysis.  Clones
CC   containing the repeat sequences were isolated by hybridisation of
CC   chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC   probe.  Over 100 repeat blocks were isolated. The inserts from the
CC   clones were amplified by primers AAT65798-T66047.  Those clones where the
CC   repeat sequence has been determined are shown in AAT65704-797.  This
CC   repeat sequence is from the marker clone Mdf34 which contains the repeat
CC   sequence having the formula: (AC)4AT(AC)15.
XX
SQ   Sequence 40 BP; 20 A; 19 C; 0 G; 1 T; 0 other;


  Query Match             0.6%;  Score 24;  DB 18;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgtgtgtgt 3872
           ||||||||||||||||||||||||
Db     24 GTGTGTGTGTGTGTATGTGTGTGT 1


RESULT   9
AAT65741/c
ID   AAT65741 standard; DNA; 50 BP.
XX
AC   AAT65741;
XX
DT   17-JUN-1997  (first entry)
XX
DE   Repeat sequence from polymorphic marker clone Mfd40.
XX
KW   Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW   PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW   linkage analysis; genetic disease; animal; plant; breeding; locus;
KW   hybridisation; chromosome; ds.
XX
OS   Homo sapiens.
XX
PN   US5582979-A.
XX
PD   10-DEC-1996.
XX
PF   21-APR-1989;   89US-0341562.
XX
PR   05-SEP-1991;   91US-0754351.
PR   21-APR-1989;   89US-0341562.
PR   04-APR-1994;   94US-0222177.
XX
PA   (MARS-) MARSHFIELD CLINIC.
XX
PI   Weber JL;
XX
DR   WPI; 1997-042299/04.
XX
PT   Detection of polymorphic genetic markers of the form
PT   (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
XX
PS   Disclosure; Column 9-10; 186pp; English.
XX
CC   The invention relates to the isolation of polymorphic repeat sequences
CC   having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC   markers.  Primers based on these sequences can be used to detect these
CC   repeats, especially for use in e.g paternity or maternity testing,
CC   human genetic analysis such as linkage analysis of genetic disease,
CC   commercial animal or plant breeding or pedigree analysis.  Clones
CC   containing the repeat sequences were isolated by hybridisation of
CC   chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC   probe.  Over 100 repeat blocks were isolated. The inserts from the
CC   clones were amplified by primers AAT65798-T66047.  Those clones where the
CC   repeat sequence has been determined are shown in AAT65704-797.  This
CC   repeat sequence is from the marker clone Mdf40 which contains the repeat
CC   sequence having the formula: (CA)13C(CA)6T(AC)5.
XX
SQ   Sequence 50 BP; 24 A; 25 C; 0 G; 1 T; 0 other;


  Query Match             0.5%;  Score 23;  DB 18;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3853 gtgtgtgtgtatgtgtgtgtgtg 3875
           |||||||||||||||||||||||
Db     50 GTGTGTGTGTATGTGTGTGTGTG 28


RESULT  10
AAQ34077
ID   AAQ34077 standard; DNA; 27 BP.
XX
AC   AAQ34077;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone TGLA47.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
```

DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
XX
PS Table 7; Page 362; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC traits esp. in cattle, to allow selective breeding.
CC See also AAQ33501-34437.
XX
SQ Sequence 27 BP; 1 A; 0 C; 13 G; 13 T; 0 other;

Query Match 0.5%; Score 22; DB 13; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3855 gtgtgtgtatgtgtgtgtgtgt 3876
||||||||||||||||||||||
Db 1 gtgtgtgtatgtgtgtgtgtgt 22

RESULT 11
AAH39357
ID AAH39357 standard; DNA; 24 BP.
XX
AC AAH39357;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific upper PCR primer SEQ ID 2153.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US28436.
XX
PR 15-OCT-1999; 99US-0160096.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample -
XX
PS Claim 1; Page 60; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence.
XX
SQ Sequence 24 BP; 1 A; 0 C; 11 G; 12 T; 0 other;

Query Match 0.5%; Score 21; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3854 tgtgtgtgtatgtgtgtgtgt 3874
|||||||||||||||||||||
Db 1 tgtgtgtgtatgtgtgtgtgt 21

RESULT 12
AAT65743/c
ID AAT65743 standard; DNA; 40 BP.
XX
AC AAT65743;
XX
DT 17-JUN-1997 (first entry)
XX
DE Repeat sequence from polymorphic marker clone Mfd42.
XX
KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW linkage analysis; genetic disease; animal; plant; breeding; locus;
KW hybridisation; chromosome; ds.
XX
OS Homo sapiens.
XX
PN US5582979-A.
XX
PD 10-DEC-1996.
XX
PF 21-APR-1989; 89US-0341562.
XX
PR 05-SEP-1991; 91US-0754351.
PR 21-APR-1989; 89US-0341562.
PR 04-APR-1994; 94US-0222177.
XX
PA (MARS-) MARSHFIELD CLINIC.
XX
PI Weber JL;
XX
DR WPI; 1997-042299/04.
XX
PT Detection of polymorphic genetic markers of the form
PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers

```
XX
PS   Disclosure; Column 9-10; 186pp; English.
XX
CC   The invention relates to the isolation of polymorphic repeat sequences
CC   having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC   markers.  Primers based on these sequences can be used to detect these
CC   repeats, especially for use in e.g paternity or maternity testing,
CC   human genetic analysis such as linkage analysis of genetic disease,
CC   commercial animal or plant breeding or pedigree analysis.  Clones
CC   containing the repeat sequences were isolated by hybridisation of
CC   chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC   probe.  Over 100 repeat blocks were isolated. The inserts from the
CC   clones were amplified by primers AAT65798-T66047.  Those clones where the
CC   repeat sequence has been determined are shown in AAT65704-797.  This
CC   repeat sequence is from the marker clone Mdf42 which contains the repeat
CC   sequence having the formula: (CA)16T(AC)3.5.
XX
SQ   Sequence 40 BP; 20 A; 19 C; 0 G; 1 T; 0 other;


  Query Match              0.5%;  Score 21;  DB 18;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 9.7;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3856 tgtgtgtatgtgtgtgtgtgt 3876
           |||||||||||||||||||||
Db     40 TGTGTGTATGTGTGTGTGTGT 20


RESULT  13
AAQ82617/c
ID   AAQ82617 standard; DNA; 20 BP.
XX
AC   AAQ82617;
XX
DT   14-SEP-1995  (first entry)
XX
DE   Chromosome 11 (locus D11S952E) STS primer 339.
XX
KW   sequence sampled mapping; genomic analysis; complex genome mapping;
KW   cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX
OS   Synthetic.
XX
PN   WO9429486-A.
XX
PD   22-DEC-1994.
XX
PF   15-JUN-1994;   94WO-US06810.
XX
PR   15-JUN-1993;   93US-0078471.
PR   07-SEP-1993;   93US-0117952.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Evans GA,  Smith MW;
XX
DR   WPI; 1995-036508/05.
XX
PT   Sequencing complex genomes, present as fragments in a cosmid
PT   library  - by sequencing end-specific nucleotides of each clone
PT   then correlating with spatial relationship of cosmid, esp. for
PT   mammalian chromosomes.
XX
PS   Example 4; Page 90; 128pp; English.
XX
CC   Sequences were determined from the ends of chromosome 11-specific
CC   cosmids by automated sequencing without intermediate subcloning.
CC   A sample of 371 DNA sequence fragments were determined and of
CC   these, 277 were suitable for STS primer prediction by computer
CC   analysis (using the "Primer" program available from E.Lander, MIT).
CC   The STSs and cosmids were mapped by in situ hybridisation, somatic
CC   cell hybrid analysis or both. Using this method, 370 STSs specific
CC   for human chromosome 11 were generated and most of them were
CC   regionally mapped. This procedure illustrates a novel method for
CC   sequencing complex genomes, designated "sequence sampled mapping".
CC   The sequence sampled mapping method is useful for the completion of
CC   high density sequence-based maps, and ultimately, for the complete
CC   sequencing of genomic DNA directly from cosmid clones.
CC   See AAQ82001-Q82706 and AAQ91325-Q91358 for STS primers.
XX
SQ   Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 other;


  Query Match              0.5%;  Score 20;  DB 16;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4119 caaactgccttcttcggaaa 4138
           ||||||||||||||||||||
Db     20 CAAACTGCCTTCTTCGGAAA 1


RESULT  14
AAQ82618
ID   AAQ82618 standard; DNA; 20 BP.
XX
AC   AAQ82618;
XX
DT   14-SEP-1995  (first entry)
XX
DE   Chromosome 11 (locus D11S952E) STS primer 340.
XX
KW   sequence sampled mapping; genomic analysis; complex genome mapping;
KW   cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX
OS   Synthetic.
XX
PN   WO9429486-A.
XX
PD   22-DEC-1994.
XX
PF   15-JUN-1994;   94WO-US06810.
XX
PR   15-JUN-1993;   93US-0078471.
PR   07-SEP-1993;   93US-0117952.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Evans GA,  Smith MW;
XX
DR   WPI; 1995-036508/05.
XX
PT   Sequencing complex genomes, present as fragments in a cosmid
PT   library  - by sequencing end-specific nucleotides of each clone
PT   then correlating with spatial relationship of cosmid, esp. for
PT   mammalian chromosomes.
XX
PS   Example 4; Page 90; 128pp; English.
XX
CC   Sequences were determined from the ends of chromosome 11-specific
CC   cosmids by automated sequencing without intermediate subcloning.
CC   A sample of 371 DNA sequence fragments were determined and of
CC   these, 277 were suitable for STS primer prediction by computer
CC   analysis (using the "Primer" program available from E.Lander, MIT).
CC   The STSs and cosmids were mapped by in situ hybridisation, somatic
CC   cell hybrid analysis or both. Using this method, 370 STSs specific
CC   for human chromosome 11 were generated and most of them were
CC   regionally mapped. This procedure illustrates a novel method for
CC   sequencing complex genomes, designated "sequence sampled mapping".
CC   The sequence sampled mapping method is useful for the completion of
CC   high density sequence-based maps, and ultimately, for the complete
CC   sequencing of genomic DNA directly from cosmid clones.
CC   See AAQ82001-Q82706 and AAQ91325-Q91358 for STS primers.
XX
SQ   Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;
```

```
  Query Match             0.5%;  Score 20;  DB 16;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4024 atcagcctagaggcctgact 4043
          ||||||||||||||||||||
Db      1 atcagcctagaggcctgact 20


RESULT  15
AAT58080/c
ID   AAT58080 standard; DNA; 21 BP.
XX
AC   AAT58080;
XX
DT   18-MAR-1997  (first entry)
XX
DE   ICAM-1 antisense oligonucleotide #10.
XX
KW   Antisense; pre-mRNA; mature mRNA; vascular defect; tissue defect;
KW   human intercellular adhesion molecule-1; ICAM-1; inflammation;
KW   adult respiratory distress syndrome; multiple organ failure; GM1594;
KW   septic shock; ss.
XX
OS   Synthetic.
XX
PN   US5580969-A.
XX
PD   03-DEC-1996.
XX
PF   24-JUL-1992;   92US-0918259.
XX
PR   12-OCT-1993;   93US-0136118.
PR   24-JUL-1992;   92US-0918259.
XX
PA   (USNA ) US SEC OF NAVY.
XX
PI   Bradley MO,  Hoke GD,  Lee C,  Williams TJ;
XX
DR   WPI; 1997-033603/03.
XX
PT   Anti-sense oligo:nucleotide(s) for blocking ICAM-1 mRNA translation
PT   - for treating septic shock, adult respiratory distress syndrome
PT   etc.
XX
PS   Claim 1; Column 21; 16pp; English.
XX
CC   The sequences given in AAT58071-85 represent oligonucleotides which are
CC   antisense to sequences contained in the pre-mRNA or mature mRNA
CC   transcript of human intercellular adhesion molecule-1 (ICAM-1).
CC   These oligonucleotides may be used for treating septic shock and the
CC   manifestations of septic shock, e.g. inflammation, and vascular and
CC   tissue defects.  They are also useful in the treatment of septic
CC   shock associated diseases, e.g. adult respiratory distress syndrome,
CC   multiple organ failure etc.
XX
SQ   Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 other;


  Query Match             0.5%;  Score 20;  DB 18;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgtgt 3868
          ||||||||||||||||||||
Db     20 GTGTGTGTGTGTGTATGTGT 1


RESULT  16
AAV38616/c
ID   AAV38616 standard; DNA; 21 BP.
XX
AC   AAV38616;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Human ICAM-1, E-selectin, VCAM-1 antisense oligonucleotide.
XX
KW   ICAM-1; intracellular adhesion molecule-; E-selectin; VCAM-1;
KW   vascular cell adhesion molecule-1; antisense; inflammatory;
KW   disease; treatment; septic shock; psoriasis; wounds; burns; acne;
KW   arthritis; organ rejection; inhibition; expression; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9824797-A1.
XX
PD   11-JUN-1998.
XX
PF   02-DEC-1996;   96WO-US19194.
XX
PR   02-DEC-1996;   96WO-US19194.
XX
PA   (DYAD-) DYAD PHARM CORP.
XX
PI   Bradley MO,  Hoke GD,  Lee C,  Williams TJ;
XX
DR   WPI; 1998-333253/29.
XX
PT   Antisense oligonucleotides to ICAM-1, E-selectin or VCAM-1 - useful
PT   for treating diseases having an inflammatory component, e.g.
PT   psoriasis, wounds and septic shock
XX
PS   Claim 8; Page 40; 48pp; English.
XX
CC   The sequence is that of an antisense oligonucleotide which is
CC   substantially complementary to at least a portion of the pre-
CC   or mature RNA transcript of human intracellular adhesion molecule
CC   (ICAM), E-selectin or vascular cell adhesion molecule (VCAM).
CC   It can be used to inhibit expression of these proteins. Inhibition
CC   of these proteins forms the basis for treatment of conditions and
CC   diseases that have an inflammatory component, e.g. acne, psoriasis,
CC   arthritis, organ rejection, wounds, burns, septic shock or
CC   inflammatory complications of septic shock.
XX
SQ   Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 other;


  Query Match             0.5%;  Score 20;  DB 19;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgtgt 3868
          ||||||||||||||||||||
Db     20 GTGTGTGTGTGTGTATGTGT 1


RESULT  17
AAA80358
ID   AAA80358 standard; DNA; 27 BP.
XX
AC   AAA80358;
XX
DT   22-NOV-2000  (first entry)
XX
DE   Human ASTH1I 5' region polymorphic site, SEQ ID NO:103 (b).
XX
KW   ASTH1 locus; ASTH1I; ASTH1J; human; chromosome 11p; asthma;
KW   bronchial hyperreactivity; ets family; transcription factor;
KW   splice variant; genetic predisposition; polymorphism; antibody;
KW   drug screening; prophylaxis; therapy; diagnosis;
KW   single nucleotide polymorphism; SNP; ss.
XX
```

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace (12..17,TA)
FT                   /*tag= a
XX
PN   US6087485-A.
XX
PD   11-JUL-2000.
XX
PF   21-JAN-1998;    98US-0009913.
XX
PR   21-JAN-1997;    97US-0035663.
PR   01-JUL-1997;    97US-0051432.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M, Miller A, North M, Cardon L, Buckler A;
PI   Brooks-Wilson AR, Carey AH;
XX
DR   WPI; 2000-505109/45.
XX
PT   New nucleic acids other than naturally occurring chromosomes encoding
PT   ASTH1 protein, for e.g. screening compositions that modulate expression
PT   or function of ASTH1 proteins or as diagnostics for genetic
PT   predisposition to asthma
XX
PS   Examples; Column 41-42; 131pp; English.
XX
CC   The invention relates to the ASTH1 locus on the short arm of human
CC   chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes,
CC   which are associated with a genetic predisposition to asthma and
CC   bronchial hyperreactivity. The ASTH1I and ASTH1J genes are oriented in
CC   opposite directions with the ASTH1 locus, and have similar patterns of
CC   expression and common sequence motifs. They are both expressed in
CC   trachea, lung and several other tissues. ASTH1I and ASTH1J are novel
CC   members of the ets family of transcription factors, which have been
CC   implicated in the activation of a variety of genes including the TCRa
CC   gene and cytokine genes known to be important in the aetiology of
CC   asthma. Both ASTH1I and ASTH1J mRNAs are alternatively spliced.
CC   Alternative splicing of transcripts has no effect on the open reading
CC   frame of ASTH1J, as the exons involved are all 5' to the start codon in
CC   exon b. In contrast, alternative splicing of ASTH1I transcripts results
CC   in 3 different ASTH1I isoforms. The invention also encompasses mouse
CC   asth1j protein. The ASTH1 nucleic acids are useful as diagnostics to
CC   identify a hereditary predisposition to asthma, as probes for identifying
CC   ASTH1 related genes, for identifying expression of the gene in a
CC   biological specimen, and for generating genetically modified non-human
CC   animals or site specific gene modifications in cell lines. The encoded
CC   ASTH1 proteins are useful as immunogens to raise specific antibodies; in
CC   drug screening for compositions that mimic or modulate activity or
CC   expression of ASTH1I and/or ASTH1J (including altered forms of these
CC   proteins); and as a therapeutic. The ASTH1 genes or fragments thereof,
CC   encoded proteins, ASTH1 genomic regulatory regions, and anti-ASTH1I and
CC   anti-ASTH1J antibodies are useful in the identification of individuals
CC   predisposed to development of asthma, and for modulation of gene activity
CC   in vivo for prophylactic and therapeutic purposes. The intact ASTH1I or
CC   ASTH1J proteins or active fragments thereof may be used to modulate or
CC   reduce bronchial hyperreactivity. Sequences AAA80260-A80261 and
CC   AAA80264-A80416 represent polymorphic sites within the ASTH1J or ASTH1I
CC   genes.
XX
SQ   Sequence 27 BP; 1 A; 2 C; 13 G; 11 T; 0 other;


  Query Match             0.5%;  Score 19;  DB 21;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3849 gtgtgtgtgtgtgtatgtg 3867
           |||||||||||||||||||
Db       3 gtgtgtgtgtgtgtatgtg 21
```

```
RESULT  18
AAQ33695
ID   AAQ33695 standard; DNA; 35 BP.
XX
AC   AAQ33695;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone TGLA127.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;    92WO-US00340.
XX
PR   15-JAN-1991;    91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M, Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 208; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised. Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000. The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM). The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 35 BP; 3 A; 1 C; 15 G; 16 T; 0 other;


  Query Match             0.5%;  Score 19;  DB 13;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3844 tgtgcgtgtgtgtgtgtgt 3862
           |||||||||||||||||||
Db       8 tgtgcgtgtgtgtgtgtgt 26


RESULT  19
AAQ33669
ID   AAQ33669 standard; DNA; 37 BP.
XX
AC   AAQ33669;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone TGLA112.
```

```
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 197; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised.  Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000.  The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM).  The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 37 BP; 1 A; 1 C; 18 G; 17 T; 0 other;


  Query Match          0.5%;  Score 19;  DB 13;  Length 37;
  Best Local Similarity  100.0%;  Pred. No. 86;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3857 gtgtgtatgtgtgtgtgtg 3875
           |||||||||||||||||||
Db      19 gtgtgtatgtgtgtgtgtg 37


RESULT  20
AAT65709/c
ID   AAT65709 standard; DNA; 46 BP.
XX
AC   AAT65709;
XX
DT   17-JUN-1997  (first entry)
XX
DE   Repeat sequence from polymorphic marker clone Mfd7.
XX
KW   Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW   PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW   linkage analysis; genetic disease; animal; plant; breeding; locus;
KW   hybridisation; chromosome; ds.
XX
OS   Homo sapiens.
XX
PN   US5582979-A.
XX
PD   10-DEC-1996.
XX
PF   21-APR-1989;   89US-0341562.
XX
PR   05-SEP-1991;   91US-0754351.
PR   21-APR-1989;   89US-0341562.
PR   04-APR-1994;   94US-0222177.
XX
PA   (MARS-) MARSHFIELD CLINIC.
XX
PI   Weber JL;
XX
DR   WPI; 1997-042299/04.
XX
PT   Detection of polymorphic genetic markers of the form
PT   (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
XX
PS   Claim 1; Column 9-10; 186pp; English.
XX
CC   The invention relates to the isolation of polymorphic repeat sequences
CC   having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC   markers.  Primers based on these sequences can be used to detect these
CC   repeats, especially for use in e.g paternity or maternity testing,
CC   human genetic analysis such as linkage analysis of genetic disease,
CC   commercial animal or plant breeding or pedigree analysis.  Clones
CC   containing the repeat sequences were isolated by hybridisation of
CC   chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC   probe.  Over 100 repeat blocks were isolated. The inserts from the
CC   clones were amplified by primers AAT65798-T66047.  Those clones where the
CC   repeat sequence has been determined are shown in AAT65704-797.  This
CC   repeat sequence is from the marker clone Mdf7 which contains the repeat
CC   sequence having the formula: (CA)20TA(CA)2.
XX
SQ   Sequence 46 BP; 23 A; 22 C; 0 G; 1 T; 0 other;


  Query Match          0.5%;  Score 19;  DB 18;  Length 46;
  Best Local Similarity  100.0%;  Pred. No. 86;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3858 tgtgtatgtgtgtgtgtgt 3876
           |||||||||||||||||||
Db      46 TGTGTATGTGTGTGTGTGT 28


RESULT  21
AAQ34167
ID   AAQ34167 standard; DNA; 50 BP.
XX
AC   AAQ34167;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Sequence of a microsatellite from clone TGLA85.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
```

```
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 397; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd.
CC   by screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised.  Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000.  The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM).  The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 50 BP; 16 A; 0 C; 8 G; 26 T; 0 other;


  Query Match             0.5%;  Score 19;  DB 13;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3852 tgtgtgtgtgtatgtgtgt 3870
           ||||||||||||||||||
Db     12 tgtgtgtgtgtatgtgtgt 30


RESULT  22
AAQ40668/c
ID   AAQ40668 standard; cDNA; 24 BP.
XX
AC   AAQ40668;
XX
DT   06-AUG-1993  (first entry)
XX
DE   tPA-12 in vitro mutagenic oligomer.
XX
KW   Blood; tissue plasminogen activator; tPA; mutein; stability; tPA-12;
KW   physiological; activity; pTB 1353; mutagenesis; plasmid; ss.
XX
OS   Synthetic.
XX
PN   JP05076361-A.
XX
PD   30-MAR-1993.
XX
PF   10-MAY-1991;   91JP-0105689.
XX
PR   10-MAY-1990;   90JP-0118710.
PR   25-DEC-1990;   90JP-0405848.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
DR   WPI; 1993-139567/17.
XX
PT   Tissue plasminogen activator mutein - useful for treating
PT   myocardial infarction and cerebral thrombosis
XX
PS   Disclosure; Page 33; 92pp; Japanese.
XX
CC   This sequence is an oligomer which was used in an oligonucleotide
CC   directed in vitro mutagenesis system for the production of tissue
CC   plasminogen activator (tPA) mutein, tPA-12.  The plasmid pTB 1353
CC   was treated with this synthetic oligomer (see also AAQ40669).  This
CC   tPA mutein has good stability in blood and good physiological
CC   activity.
XX
SQ   Sequence 24 BP; 6 A; 3 C; 9 G; 6 T; 0 other;


  Query Match             0.4%;  Score 18;  DB 14;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    616 ttgccaagcacctactat 633
          ||||||||||||||||||
Db     23 TTGCCAAGCACCTACTAT 6


RESULT  23
AAZ98502/c
ID   AAZ98502 standard; DNA; 30 BP.
XX
AC   AAZ98502;
XX
DT   19-JUN-2000  (first entry)
XX
DE   H. discus derived sequence #20.
XX
KW   Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
KW   Haliotis discus; ss.
XX
OS   Haliotis discus.
XX
PN   WO200011156-A1.
XX
PD   02-MAR-2000.
XX
PF   01-JUL-1999;   99WO-JP03551.
XX
PR   18-AUG-1998;   98JP-0232153.
XX
PA   (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
XX
PI   Takahashi H,  Sekino M;
XX
DR   WPI; 2000-224692/19.
XX
PT   Isolation of satellite sequences from genomic DNA for use as DNA
PT   markers comprises isolating a library with high homogeneity by DNA
PT   fragmentation -
XX
PS   Example 5; Page 14; 35pp; Japanese.
XX
CC   The invention provides a novel method for isolation of satellite
CC   sequences from genomic DNA that comprises fragmentation of the DNA by
CC   a method which is not dependent on base sequences, then selection of
CC   the satellite sequences from the obtained genomic library of high
CC   homogeneity. The method is useful for the isolation of microsatellite
CC   DNA sequences which can be used as DNA markers. The new method markedly
CC   improves the efficiency of isolation of satellite sequences in
CC   comparison to prior art methods which are reliant on base sequences.
CC   Sequences AAZ98483-514 represent sequences from Haliotis discus, used in
CC   the method of the invention.
XX
SQ   Sequence 30 BP; 15 A; 13 C; 0 G; 2 T; 0 other;


  Query Match             0.4%;  Score 18;  DB 21;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgt 3866
          ||||||||||||||||||
Db     19 GTGTGTGTGTGTGTATGT 2


RESULT  24
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```
AAQ34119
ID   AAQ34119 standard; DNA; 32 BP.
XX
AC   AAQ34119;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Sequence of a microsatellite from clone TGLA67.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 378; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd.
CC   by screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised.  Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000.  The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM).  The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 32 BP; 0 A; 1 C; 16 G; 15 T; 0 other;


  Query Match             0.4%;  Score 18;  DB 13;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3844 tgtgcgtgtgtgtgtgtg 3861
           ||||||||||||||||||
Db     15 tgtgcgtgtgtgtgtgtg 32


RESULT  25
AAQ33698
ID   AAQ33698 standard; DNA; 37 BP.
XX
AC   AAQ33698;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone TGLA128.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 209; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised.  Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000.  The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM).  The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 37 BP; 2 A; 1 C; 15 G; 19 T; 0 other;


  Query Match             0.4%;  Score 18;  DB 13;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgt 3866
           ||||||||||||||||||
Db     20 gtgtgtgtgtgtgtatgt 37


RESULT  26
AAT65788/c
ID   AAT65788 standard; DNA; 43 BP.
XX
AC   AAT65788;
XX
DT   17-JUN-1997  (first entry)
XX
DE   Repeat sequence from polymorphic marker clone Mfd117.
XX
KW   Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW   PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW   linkage analysis; genetic disease; animal; plant; breeding; locus;
KW   hybridisation; chromosome; ds.
XX
OS   Homo sapiens.
XX
PN   US5582979-A.
XX
PD   10-DEC-1996.
XX
```

```
PF   21-APR-1989;   89US-0341562.
XX
PR   05-SEP-1991;   91US-0754351.
PR   21-APR-1989;   89US-0341562.
PR   04-APR-1994;   94US-0222177.
XX
PA   (MARS-) MARSHFIELD CLINIC.
XX
PI   Weber JL;
XX
DR   WPI; 1997-042299/04.
XX
PT   Detection of polymorphic genetic markers of the form
PT   (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
XX
PS   Claim 1; Column 13-14; 186pp; English.
XX
CC   The invention relates to the isolation of polymorphic repeat sequences
CC   having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC   markers.  Primers based on these sequences can be used to detect these
CC   repeats, especially for use in e.g paternity or maternity testing,
CC   human genetic analysis such as linkage analysis of genetic disease,
CC   commercial animal or plant breeding or pedigree analysis.  Clones
CC   containing the repeat sequences were isolated by hybridisation of
CC   chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC   probe.  Over 100 repeat blocks were isolated. The inserts from the
CC   clones were amplified by primers AAT65798-T66047.  Those clones where the
CC   repeat sequence has been determined are shown in AAT65704-797.  This
CC   repeat sequence is from the marker clone Mdf117 which contains the
CC   repeat sequence having the formula: GCAGCAACAT(AC)16.5.
XX
SQ   Sequence 43 BP; 21 A; 19 C; 2 G; 1 T; 0 other;


  Query Match             0.4%;  Score 18;  DB 18;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatgt 3866
           ||||||||||||||||||
Db     24 GTGTGTGTGTGTGTATGT 7


RESULT  27
AAZ98507/c
ID   AAZ98507 standard; DNA; 44 BP.
XX
AC   AAZ98507;
XX
DT   19-JUN-2000  (first entry)
XX
DE   H. discus derived sequence #25.
XX
KW   Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
KW   Haliotis discus; ss.
XX
OS   Haliotis discus.
XX
PN   WO200011156-A1.
XX
PD   02-MAR-2000.
XX
PF   01-JUL-1999;   99WO-JP03551.
XX
PR   18-AUG-1998;   98JP-0232153.
XX
PA   (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
XX
PI   Takahashi H,  Sekino M;
XX
DR   WPI; 2000-224692/19.
XX
PT   Isolation of satellite sequences from genomic DNA for use as DNA
PT   markers comprises isolating a library with high homogeneity by DNA
PT   fragmentation -
XX
PS   Example 5; Page 14; 35pp; Japanese.
XX
CC   The invention provides a novel method for isolation of satellite
CC   sequences from genomic DNA that comprises fragmentation of the DNA by
CC   a method which is not dependent on base sequences, then selection of
CC   the satellite sequences from the obtained genomic library of high
CC   homogeneity. The method is useful for the isolation of microsatellite
CC   DNA sequences which can be used as DNA markers. The new method markedly
CC   improves the efficiency of isolation of satellite sequences in
CC   comparison to prior art methods which are reliant on base sequences.
CC   Sequences AAZ98483-514 represent sequences from Haliotis discus, used in
CC   the method of the invention.
XX
SQ   Sequence 44 BP; 17 A; 20 C; 7 G; 0 U; 0 other;


  Query Match             0.4%;  Score 18;  DB 21;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3845 gtgcgtgtgtgtgtgtgt 3862
           ||||||||||||||||||
Db     19 GTGCGTGTGTGTGTGTGT 2


RESULT  28
AAA80357
ID   AAA80357 standard; DNA; 23 BP.
XX
AC   AAA80357;
XX
DT   22-NOV-2000  (first entry)
XX
DE   Human ASTH1I 5' region polymorphic site, SEQ ID NO:103 (a).
XX
KW   ASTH1 locus; ASTH1I; ASTH1J; human; chromosome 11p; asthma;
KW   bronchial hyperreactivity; ets family; transcription factor;
KW   splice variant; genetic predisposition; polymorphism; antibody;
KW   drug screening; prophylaxis; therapy; diagnosis;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace (12..13,TGTGTA)
FT                   /*tag= a
XX
PN   US6087485-A.
XX
PD   11-JUL-2000.
XX
PF   21-JAN-1998;   98US-0009913.
XX
PR   21-JAN-1997;   97US-0035663.
PR   01-JUL-1997;   97US-0051432.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  North M,  Cardon L,  Buckler A;
PI   Brooks-Wilson AR,  Carey AH;
XX
DR   WPI; 2000-505109/45.
XX
PT   New nucleic acids other than naturally occurring chromosomes encoding
PT   ASTH1 protein, for e.g. screening compositions that modulate expression
PT   or function of ASTH1 proteins or as diagnostics for genetic
PT   predisposition to asthma -
XX
PS   Examples; Column 41-42; 131pp; English.
XX
```

```
CC   The invention relates to the ASTH1 locus on the short arm of human
CC   chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes,
CC   which are associated with a genetic predisposition to asthma and
CC   bronchial hyperreactivity. The ASTH1I and ASTH1J genes are oriented in
CC   opposite directions with the ASTH1 locus, and have similar patterns of
CC   expression and common sequence motifs. They are both expressed in
CC   trachea, lung and several other tissues. ASTH1I and ASTH1J are novel
CC   members of the ets family of transcription factors, which have been
CC   implicated in the activation of a variety of genes including the TCRa
CC   gene and cytokine genes known to be important in the aetiology of
CC   asthma. Both ASTH1I and ASTH1J mRNAs are alternatively spliced.
CC   Alternative splicing of transcripts has no effect on the open reading
CC   frame of ASTH1J, as the exons involved are all 5' to the start codon in
CC   exon b. In contrast, alternative splicing of ASTH1I transcripts results
CC   in 3 different ASTH1I isoforms. The invention also encompasses mouse
CC   asth1j protein. The ASTH1 nucleic acids are useful as diagnostics to
CC   identify a hereditary predisposition to asthma, as probes for identifying
CC   ASTH1 related genes, for identifying expression of the gene in a
CC   biological specimen, and for generating genetically modified non-human
CC   animals or site specific gene modifications in cell lines. The encoded
CC   ASTH1 proteins are useful as immunogens to raise specific antibodies; in
CC   drug screening for compositions that mimic or modulate activity or
CC   expression of ASTH1I and/or ASTH1J (including altered forms of these
CC   proteins); and as a therapeutic. The ASTH1 genes or fragments thereof,
CC   encoded proteins, ASTH1 genomic regulatory regions, and anti-ASTH1I and
CC   anti-ASTH1J antibodies are useful in the identification of individuals
CC   predisposed to development of asthma, and for modulation of gene activity
CC   in vivo for prophylactic and therapeutic purposes. The intact ASTH1I or
CC   ASTH1J proteins or active fragments thereof may be used to modulate or
CC   reduce bronchial hyperreactivity. Sequences AAA80260-A80261 and
CC   AAA80264-A80416 represent polymorphic sites within the ASTH1J or ASTH1I
CC   genes.
XX
SQ   Sequence 23 BP; 1 A; 2 C; 11 G; 9 T; 0 other;

  Query Match             0.4%;  Score 17;  DB 21;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3851 gtgtgtgtgtgtatgtg 3867
            |||||||||||||||||
Db      1 gtgtgtgtgtgtatgtg 17


RESULT  29
AAZ92012/c
ID   AAZ92012 standard; DNA; 25 BP.
XX
AC   AAZ92012;
XX
DT   08-JUN-2000  (first entry)
XX
DE   Mahogany protein gene exon 28+UTR primer CelegE168.
XX
KW   Mahogany gene; mouse; mg gene; regulatory defect; gene therapy; obesity;
KW   weight regulation; cell therapy; body weight disorder; cachexia;
KW   anorexia; hyperpigmentation; increased metabolic rate disorder;
KW   hyperphagia; Antiobesity; antianorexic; anticachexic; PCR primer; ss.
XX
OS   Mammalia.
XX
PN   WO200005373-A2.
XX
PD   03-FEB-2000.
XX
PF   21-JUL-1999;   99WO-US16484.
XX
PR   21-JUL-1998;   98US-0093630.
PR   20-OCT-1998;   98US-0104978.
PR   05-FEB-1999;   99US-0245041.
XX
PA   (MILL-) MILLENIUM PHARM INC.
XX
PI   Moore K,  Nagle DL;
XX
DR   WPI; 2000-195103/17.
XX
PT   New human and murine mahogany genes, useful, e.g. for diagnosis and
PT   treatment of body weight disorders -
XX
PS   Example; Fig 5; 188pp; English.
XX
CC   This sequence represents a PCR primer for a mahogany gene of the
CC   invention. The mahogany genes are used: (i) to produce recombinant
CC   mahogany (mg) proteins (II); (ii) as a source of antisense, ribozyme or
CC   triplex-forming therapeutics; (iii) as a source of diagnostic probes and
CC   primers for detecting expression of mg genes or mutations, regulatory
CC   defects, in this gene, or for isolation of related sequences; and
CC   (iv) in (cell-based) gene therapy. (II) are used to raise specific
CC   antibodies (Ab); to identify other (extra)cellular products involved in
CC   weight regulation, and to screen for agents that disrupt interaction
CC   between (II) and other macromolecules. The Ab are used to detect abnormal
CC   levels (or function) of (II) (for diagnosis, prognosis or monitoring of
CC   treatment); to evaluate (II)-expressing cells intended for cell therapy,
CC   and as therapeutic mg inhibitors. Cells that express the mg gene (or
CC   contain the mg polypeptide) are used to identify agents (A) that modulate
CC   mg activity. (A) are potentially useful for the treatment of body weight
CC   disorders, particularly obesity, cachexia or anorexia, or other
CC   conditions associated with the mg gene such as hyperpigmentation,
CC   hyperphagia and disorders that result in increased metabolic rate.
XX
SQ   Sequence 25 BP; 10 A; 10 C; 2 G; 3 T; 0 other;

  Query Match             0.4%;  Score 17;  DB 21;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3853 gtgtgtgtgtatgtgtg 3869
            |||||||||||||||||
Db     17 GTGTGTGTGTATGTGTG 1


RESULT  30
AAQ34094
ID   AAQ34094 standard; DNA; 40 BP.
XX
AC   AAQ34094;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Sequence of a microsatellite from clone TGLA53.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
```

PS Table 7; Page 369; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd.
CC by screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC traits esp. in cattle, to allow selective breeding.
CC See also AAQ33501-34437.
XX
SQ Sequence 40 BP; 7 A; 1 C; 13 G; 19 T; 0 other;

Query Match 0.4%; Score 17; DB 13; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3844 tgtgcgtgtgtgtgtgt 3860
||||||||||||||||
Db 9 tgtgcgtgtgtgtgtgt 25

RESULT 31
AAZ98493/c
ID AAZ98493 standard; DNA; 40 BP.
XX
AC AAZ98493;
XX
DT 19-JUN-2000 (first entry)
XX
DE H. discus derived sequence #11.
XX
KW Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
KW Haliotis discus; ss.
XX
OS Haliotis discus.
XX
PN WO200011156-A1.
XX
PD 02-MAR-2000.
XX
PF 01-JUL-1999; 99WO-JP03551.
XX
PR 18-AUG-1998; 98JP-0232153.
XX
PA (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
XX
PI Takahashi H, Sekino M;
XX
DR WPI; 2000-224692/19.
XX
PT Isolation of satellite sequences from genomic DNA for use as DNA
PT markers comprises isolating a library with high homogeneity by DNA
PT fragmentation -
XX
PS Example 5; Page 14; 35pp; Japanese.
XX
CC The invention provides a novel method for isolation of satellite
CC sequences from genomic DNA that comprises fragmentation of the DNA by
CC a method which is not dependent on base sequences, then selection of
CC the satellite sequences from the obtained genomic library of high
CC homogeneity. The method is useful for the isolation of microsatellite
CC DNA sequences which can be used as DNA markers. The new method markedly
CC improves the efficiency of isolation of satellite sequences in
CC comparison to prior art methods which are reliant on base sequences.
CC Sequences AAZ98483-514 represent sequences from Haliotis discus, used in
CC the method of the invention.
XX
SQ Sequence 40 BP; 19 A; 19 C; 0 G; 2 T; 0 other;

Query Match 0.4%; Score 17; DB 21; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3860 tgtatgtgtgtgtgtgt 3876
||||||||||||||||
Db 40 TGTATGTGTGTGTGTGT 24

RESULT 32
AAT65797/c
ID AAT65797 standard; DNA; 42 BP.
XX
AC AAT65797;
XX
DT 17-JUN-1997 (first entry)
XX
DE Repeat sequence from polymorphic marker clone Mfd1.
XX
KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW linkage analysis; genetic disease; animal; plant; breeding; locus;
KW hybridisation; chromosome; ds.
XX
OS Homo sapiens.
XX
PN US5582979-A.
XX
PD 10-DEC-1996.
XX
PF 21-APR-1989; 89US-0341562.
XX
PR 05-SEP-1991; 91US-0754351.
PR 21-APR-1989; 89US-0341562.
PR 04-APR-1994; 94US-0222177.
XX
PA (MARS-) MARSHFIELD CLINIC.
XX
PI Weber JL;
XX
DR WPI; 1997-042299/04.
XX
PT Detection of polymorphic genetic markers of the form
PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
XX
PS Claim 1; Column 9-10; 186pp; English.
XX
CC The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g paternity or maternity testing,
CC human genetic analysis such as linkage analysis of genetic disease,
CC commercial animal or plant breeding or pedigree analysis. Clones
CC containing the repeat sequences were isolated by hybridisation of
CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC probe. Over 100 repeat blocks were isolated. The inserts from the
CC clones were amplified by primers AAT65798-T66047. Those clones where the
CC repeat sequence has been determined are shown in AAT65704-797. This
CC repeat sequence is from the marker clone Mdf1 which contains the repeat
CC sequence having the formula: CATA(CA)19.
XX
SQ Sequence 42 BP; 21 A; 20 C; 0 G; 1 T; 0 other;

Query Match 0.4%; Score 17; DB 18; Length 42;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

```
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtatg 3865
          |||||||||||||||||
Db     17 GTGTGTGTGTGTGTATG 1


RESULT  33
AAZ68141/c
ID   AAZ68141 standard; DNA; 47 BP.
XX
AC   AAZ68141;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:2488.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,C)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome -
XX
PS   Claim 3; Page 761; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 23 A; 9 C; 2 G; 13 T; 0 other;


  Query Match             0.4%;  Score 17;  DB 21;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3862 tatgtgtgtgtgtgtat 3878
          |||||||||||||||||
Db     25 TATGTGTGTGTGTGTAT 9


RESULT  34
AAQ34122
ID   AAQ34122 standard; DNA; 49 BP.
XX
AC   AAQ34122;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Sequence of a microsatellite from clone TGLA68.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 379; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd.
CC   by screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised.  Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000.  The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM).  The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 49 BP; 7 A; 0 C; 17 G; 25 T; 0 other;


  Query Match             0.4%;  Score 17;  DB 13;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3860 tgtatgtgtgtgtgtgt 3876
          |||||||||||||||||
Db      1 tgtatgtgtgtgtgtgt 17


RESULT  35
AAT30412
ID   AAT30412 standard; DNA; 19 BP.
XX
AC   AAT30412;
```

```
XX
DT   28-JAN-1997  (first entry)
XX
DE   Compound simple sequence repeat primer (GT)7.5(AT)2.
XX
KW   Detection; polymorphism; perfect compound simple sequence repeat;
KW   adaptor directed primer; genome; genetic; fingerprinting;
KW   amplified fragment length polymorphism assay;
KW   microsatellite region; genetic trait marking;
KW   germplasm comparisons; compound; ss.
XX
OS   Synthetic.
XX
PN   WO9617082-A2.
XX
PD   06-JUN-1996.
XX
PF   21-NOV-1995;   95WO-US15150.
XX
PR   28-NOV-1994;   94US-0346456.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Morgante M,  Vogel JM;
XX
DR   WPI; 1996-277795/28.
XX
PT   Modified amplified fragment length polymorphism assay - for
PT   detection of polymorphism esp. in micro:satellite regions
XX
PS   Example 2; Page 84; 173pp; English.
XX
CC   Detecting polymorphisms between 2 nucleic acid samples, esp. in
CC   microsatellite regions, comprises digesting the nucleic acid to
CC   generate fragments, ligating adaptor segments to their ends,
CC   amplifying them using primer directed amplification and comparing
CC   the prods. to detect differences. The primers used in the
CC   amplification comprise a primer consisting of a perfect cpd. simple
CC   sequence repeat (SSR), and an adaptor directed primer, comprising a
CC   sequence complementary to an adaptor segment. The present sequence
CC   is an example of a compound SSR primer.
CC   The method represents a modified amplified fragment length
CC   polymorphism assay, which is partic. useful for genome
CC   fingerprinting, i.e. for genetic trait marking and germplasm
CC   comparisons.
XX
SQ   Sequence 19 BP; 2 A; 0 C; 7 G; 10 T; 0 other;


  Query Match             0.4%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtat 3864
           ||||||||||||||||
Db      2 gtgtgtgtgtgtgtat 17


RESULT  36
AAV41067/c
ID   AAV41067 standard; DNA; 19 BP.
XX
AC   AAV41067;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Primer TEL:114U19 for abnormality detection.
XX
KW   PCR primer; chromosomal abnormality; abnormality detection; leukaemia;
KW   lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;
KW   medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
XX
OS   Synthetic.
```

```
OS   Homo sapiens.
XX
PN   WO9824928-A2.
XX
PD   11-JUN-1998.
XX
PF   08-DEC-1997;   97WO-DK00556.
XX
PR   06-DEC-1996;   96DK-0001401.
XX
PA   (PALL/) PALLISGAARD N.
XX
PI   Hokland P,  Pallisgaard N;
XX
DR   WPI; 1998-333344/29.
XX
PT   Detection of chromosomal abnormalities - by subjecting patient
PT   sample nucleic acids to a multiplex molecular amplification
PT   procedure using primers specific for characteristic nucleic acid
PT   sequence
XX
PS   Claim 73; Page 107; 126pp; English.
XX
CC   This sequence represents a primer used in the method of the invention for
CC   the detection of the presence or absence of chromosomal abnormalities,
CC   each abnormality being associated with a condition in a subject and each
CC   being defined by at least one characteristic nucleic acid sequence. The
CC   method comprises: (a) obtaining a sample of nucleic acids derived from a
CC   subject which may harbour one of the chromosomal abnormalities;
CC   (b) subjecting the sample to a multiplex molecular amplification (MMA)
CC   procedure, where a number of the characteristic sequences, if present in
CC   a sufficient amount, will be amplified; (c) retrieving the product(s)
CC   from step (b), and detecting the presence and/or absence of an amplicon
CC   characteristic of the abnormal sequences to detect the presence or
CC   absence of corresponding chromosomal abnormalities; where the MMA
CC   procedure comprises the use of at least 7 mutually distinct primers (MDP)
CC   in one single reaction mixture, each of the primers defining an end of at
CC   least one characteristic nucleic acid sequence, and where at least one of
CC   the primers defines the first end of at least two characteristic nucleic
CC   acid sequences, the characteristic nucleic acid sequences each being
CC   determined in their opposite ends by MDP selected from the remainder of
CC   the MDP. The methods can be used for detecting chromosomal abnormalities
CC   associated with diseases including numerous leukaemia's, lymphoma's,
CC   carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,
CC   medullablastoma, malignant melanoma, and malignant neoplastic conditions.
XX
SQ   Sequence 19 BP; 4 A; 7 C; 3 G; 5 T; 0 other;


  Query Match             0.4%;  Score 16;  DB 19;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1701 tggaacatgaagtggc 1716
           ||||||||||||||||
Db     19 TGGAACATGAAGTGGC 4


RESULT  37
AAQ48546/c
ID   AAQ48546 standard; DNA; 20 BP.
XX
AC   AAQ48546;
XX
DT   22-FEB-1994  (first entry)
XX
DE   HPV E6/7 region probe.
XX
KW   Human papilloma virus; HPV; E6; E7; benign; malignant; probe; ss.
XX
OS   Synthetic.
XX
PN   JP05192200-A.
```

```
XX
PD   03-AUG-1993.
XX
PF   19-AUG-1991;   91JP-0230839.
XX
PR   20-AUG-1990;   90JP-0217067.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1993-277497/35.
XX
PT   Detecting benign and/or malignant human papilloma virus - by
PT   detecting DNA sequence of E6 and/or E7 region of human papilloma
PT   virus
XX
PS   Disclosure; Page 14; 18pp; Japanese.
XX
CC   The probe is used to detect benign and/or malignant human papilloma
CC   virus. The probe binds to the E6 and/or E7 region of the virus.
XX
SQ   Sequence 20 BP; 6 A; 6 C; 3 G; 5 T; 0 other;


  Query Match             0.4%;  Score 16;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2382 tgtccagcagtgtaag 2397
           ||||||||||||||||
Db     16 TGTCCAGCAGTGTAAG 1


RESULT  38
AAT30427/c
ID   AAT30427 standard; DNA; 20 BP.
XX
AC   AAT30427;
XX
DT   28-JAN-1997  (first entry)
XX
DE   Compound simple sequence repeat primer (CA)4.5(TA)7.5.
XX
KW   Detection; polymorphism; perfect compound simple sequence repeat;
KW   adaptor directed primer; genome; genetic; fingerprinting;
KW   amplified fragment length polymorphism assay;
KW   microsatellite region; genetic trait marking;
KW   germplasm comparisons; compound; ss.
XX
OS   Synthetic.
XX
PN   WO9617082-A2.
XX
PD   06-JUN-1996.
XX
PF   21-NOV-1995;   95WO-US15150.
XX
PR   28-NOV-1994;   94US-0346456.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Morgante M,  Vogel JM;
XX
DR   WPI; 1996-277795/28.
XX
PT   Modified amplified fragment length polymorphism assay - for
PT   detection of polymorphism esp. in micro:satellite regions
XX
PS   Disclosure; Fig 1c; 173pp; English.
XX
CC   Detecting polymorphisms between 2 nucleic acid samples, esp. in
CC   microsatellite regions, comprises digesting the nucleic acid to
CC   generate fragments, ligating adaptor segments to their ends,
CC   amplifying them using primer directed amplification and comparing
CC   the prods. to detect differences. The primers used in the
CC   amplification comprise a primer consisting of a perfect cpd. simple
CC   sequence repeat (SSR), and an adaptor directed primer, comprising a
CC   sequence complementary to an adaptor segment. The present sequence
CC   is an example of a compound SSR primer.
CC   The method represents a modified amplified fragment length
CC   polymorphism assay, which is partic. useful for genome
CC   fingerprinting, i.e. for genetic trait marking and germplasm
CC   comparisons.
XX
SQ   Sequence 20 BP; 10 A; 7 C; 0 G; 3 T; 0 other;


  Query Match             0.4%;  Score 16;  DB 17;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3849 gtgtgtgtgtgtgtat 3864
           ||||||||||||||||
Db     19 GTGTGTGTGTGTGTAT 4


RESULT  39
AAS09069
ID   AAS09069 standard; DNA; 20 BP.
XX
AC   AAS09069;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human MEKK2 antisense oligonucleotide 113875.
XX
KW   Human; mitogen-activated protein kinase kinase kinase 2; MAP; MEKK2;
KW   MEK kinase 2; MAP/ERK kinase kinase 2; immunological disorder;
KW   inflammatory disorder; hyperproliferative disorder; cancer; antisense;
KW   phosphorothioate; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..20
FT                    /*tag= a
FT                    /mod_base= "OTHER"
FT                    /note= "OTHER= phosphorothioate internucleotide linkages.
FT                          Some bases especially bases 1-5 and bases 16-20
FT                          are 2'-methoxyethyl (2'-MOE) bases, bases 6-15
FT                          are 2'-deoxynucleotides and all cytidine bases
FT                          are 5'-methylcytidines"
XX
PN   WO200152863-A1.
XX
PD   26-JUL-2001.
XX
PF   16-JAN-2001; 2001WO-US01361.
XX
PR   20-JAN-2000; 2000US-0488744.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Gaarde WA,  Ward DT,  Freier SM,  Wyatt JR;
XX
DR   WPI; 2001-442246/47.
XX
PT   Antisense compound 8 to 30 nucleobases in length targeted to a nucleic
PT   acid molecule encoding MEKK2, useful for the treatment of an
PT   immunological,inflammatory of hyperproliferative disorder -
XX
PS   Claim 3; Page 79; 105pp; English.
XX
CC   The present sequence for human MEKK2 antisense oligonucleotide 113875
CC   is 1 of various novel human mitogen-activated protein (MAP)
CC   kinase kinase kinase 2 (MEKK2, also known as MEK kinase 2 and
CC   MAP/ERK kinase kinase 2) antisense oligonucleotides (AAS09045-AAS09122)
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CC   which specifically hybridise with and inhibit the expression of MEKK2.
CC   The antisense oligonucleotides can be used in a composition to modulate
CC   the expression of MEKK2 (AAU03598). The antisense oligonucleotides are
CC   useful for inhibiting the expression of MEKK2 in the treatment of
CC   immunological disorders, inflammatory disorders and hyperproliferative
CC   disorders e.g. cancer.
XX
SQ   Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 other;


  Query Match             0.4%;  Score 16;  DB 22;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2545 tctggtttcctgcaag 2560
           ||||||||||||||||
Db      5 tctggtttcctgcaag 20


RESULT  40
AAC83579/c
ID   AAC83579 standard; DNA; 23 BP.
XX
AC   AAC83579;
XX
DT   28-FEB-2001  (first entry)
XX
DE   Human FMR1 gene triplet repeat PCR primer NM-BS-for.
XX
KW   Human; FMR1; FMRP; Fragile X syndrome; methylation; diagnosis;
KW   chromosome Xq27.3; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6143504-A.
XX
PD   07-NOV-2000.
XX
PF   27-OCT-1999;   99US-0429499.
XX
PR   27-OCT-1999;   99US-0429499.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Das S,  Ledbetter DH;
XX
DR   WPI; 2001-006432/01.
XX
PT   Determining methylation state of FMR1 gene promoter for diagnosing
PT   fragile X syndrome in males involves denaturing DNA sample, subjecting
PT   DNA to bisulfite modification, amplifying DNA and detecting products
XX
PS   Claim 17; Column 31; 20pp; English.
XX
CC   The present invention describes a novel method of diagnosing Fragile X
CC   syndrome using a PCR-based method of methylation analysis. The FMR1 gene
CC   promoter, located at chromosome Xq27.3, is composed of a CGG
CC   trinucleotide repeat. The expansion of this repeat leads to a premutation
CC   and then a full mutation, the latter of which is likely to cause the
CC   methylation of a nearby CpG island, causing the Fragile X syndrome
CC   phenotype. This method is useful in the design of appropriate therapies
CC   and counselling for affected individuals and carriers.
XX
SQ   Sequence 23 BP; 11 A; 10 C; 0 G; 2 T; 0 other;


  Query Match             0.4%;  Score 16;  DB 22;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3855 gtgtgtgtatgtgtgt 3870
           ||||||||||||||||
Db     16 GTGTGTGTATGTGTGT 1


RESULT  41
AAZ98498/c
ID   AAZ98498 standard; DNA; 24 BP.
XX
AC   AAZ98498;
XX
DT   19-JUN-2000  (first entry)
XX
DE   H. discus derived sequence #16.
XX
KW   Satellite sequence; DNA fragmentation; microsatelbite DNA; DNA marker;
KW   Haliotis discus; ss.
XX
OS   Haliotis discus.
XX
PN   WO200011156-A1.
XX
PD   02-MAR-2000.
XX
PF   01-JUL-1999;   99WO-JP03551.
XX
PR   18-AUG-1998;   98JP-0232153.
XX
PA   (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
XX
PI   Takahashi H;  Sekino M;
XX
DR   WPI; 2000-224692/19.
XX
PT   Isolation of satellite sequences from genomic DNA for use as DNA
PT   markers comprises isolating a library with high homogeneity by DNA
PT   fragmentation -
XX
PS   Example 5; Page 14; 35pp; Japanese.
XX
CC   The invention provides a novel method for isolation of satellite
CC   sequences from genomic DNA that comprises fragmentation of the DNA by
CC   a method which is not dependent on base sequences, then selection of
CC   the satellite sequences from the obtained genomic library of high
CC   homogeneity. The method is useful for the isolation of microsatellite
CC   DNA sequences which can be used as DNA markers. The new method markedly
CC   improves the efficiency of isolation of satellite sequences in
CC   comparison to prior art methods which are reliant on base sequences.
CC   Sequences AAZ98483-514 represent sequences from Haliotis discus, used in
CC   the method of the invention.
XX
SQ   Sequence 24 BP; 8 A; 12 C; 4 G; 0 U; 0 other;


  Query Match             0.4%;  Score 16;  DB 21;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3847 gcgtgtgtgtgtgtgt 3862
           ||||||||||||||||
Db     19 GCGTGTGTGTGTGTGT 4


RESULT  42
AAQ34131
ID   AAQ34131 standard; DNA; 26 BP.
XX
AC   AAQ34131;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Sequence of a microsatellite from clone TGLA70B.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
```

OS Bos taurus.
XX
PN WO9213102-A.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US00340.
XX
PR 15-JAN-1991; 91US-0642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
XX
PS Table 7; Page 383; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd.
CC by screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC traits esp. in cattle, to allow selective breeding.
CC See also AAQ33501-34437.
XX
SQ Sequence 26 BP; 2 A; 1 C; 12 G; 11 T; 0 other;

Query Match 0.4%; Score 16; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3847 gcgtgtgtgtgtgtgt 3862
||||||||||||||||
Db 7 gcgtgtgtgtgtgtgt 22

RESULT 43
AAQ33740
ID AAQ33740 standard; DNA; 27 BP.
XX
AC AAQ33740;
XX
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA154.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US00340.
XX
PR 15-JAN-1991; 91US-0642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
XX
PS Table 7; Page 226; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC traits esp. in cattle, to allow selective breeding.
CC See also AAQ33501-34437.
XX
SQ Sequence 27 BP; 2 A; 0 C; 12 G; 13 T; 0 other;

Query Match 0.4%; Score 16; DB 13; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3849 gtgtgtgtgtgtgtat 3864
||||||||||||||||
Db 4 gtgtgtgtgtgtgtat 19

RESULT 44
AAI61970/c
ID AAI61970 standard; DNA; 27 BP.
XX
AC AAI61970;
XX
DT 16-OCT-2001 (first entry)
XX
DE Soybean 240017 region G3 DNA forward primer, SEQ ID NO: 601.
XX
KW Soybean; antihelmintic; gene therapy; soybean cyst nematode; SCN;
KW SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;
KW 240017 region G3; 318013 region A3; 515002 region G2; PCR primer; ss.
XX
OS Glycine max.
XX
PN WO200151627-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US00552.
XX
PR 07-JAN-2000; 2000US-0174880.
XX
PA (MONS) MONSANTO CO.
XX
PI Hauge BM, Wang ML, Parsons JD, Parnell LD;
XX
DR WPI; 2001-425872/45.
XX
PT New purified nucleic acid for producing a soybean plant having soybean
PT cyst nematode resistance and for use in plant breeding programs -
XX

PS Claim 25; Page 1178; 1353pp; English.
XX
CC The invention relates to nucleic acid molecules from regions of the
CC soybean genome which are associated with soybean cyst nematode (SCN)
CC resistance. The nucleic acids are used to transform plants, and can
CC produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.
CC The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes
CC of soybean plants and for introgressing SCN resistance or partial SCN
CC resistance into soybean plants. They can also be used in plant breeding
CC programmes. The invention also relates to proteins encoded by such
CC nucleic acid molecules, as well as antibodies capable of recognising
CC these proteins. The present sequence is a primer used to amplify a
CC region of the soybean genome.
XX
SQ Sequence 27 BP; 12 A; 11 C; 0 G; 4 T; 0 other;

Query Match 0.4%; Score 16; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3849 gtgtgtgtgtgtgtat 3864
||||||||||||||||
Db 22 GTGTGTGTGTGTGTAT 7

RESULT 45
AAQ33761
ID AAQ33761 standard; DNA; 34 BP.
XX
AC AAQ33761;
XX
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA170.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US00340.
XX
PR 15-JAN-1991; 91US-0642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
XX
PS Table 7; Page 234; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC traits esp. in cattle, to allow selective breeding.
CC See also AAQ33501-34437.
XX
SQ Sequence 34 BP; 0 A; 2 C; 17 G; 15 T; 0 other;

Query Match 0.4%; Score 16; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3847 gcgtgtgtgtgtgtgt 3862
||||||||||||||||
Db 13 gcgtgtgtgtgtgtgt 28

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Job time: 9828 sec